NUCLEOTIDE AND PREDICTED TRANSLATION PRODUCT
FOR HUMAN HEPATOMA DERIVED GROWTH FACTOR-LIKE PROTEIN (HDGF-2)

```
   1 GAATTCGTGCTCTTAGGGTGGTTGGGTGGTAAGATGGCGGCTGTGAGTCTGCGGCTCGGC
                                       M  A  A  V  S  L  R  L  G
  61 GACTTGGTGTGGGGGAAACTCGGCCGATATCCTCCTTGGCCAGGAAAGATTGTTAATCCA
     D  L  V  W  G  K  L  G  R  Y  P  P  W  P  G  K  I  V  N  P
 121 CCAAAGGACTTGAAGAAACCTCGCGGAAAGAAATGCTTCTTTGTGAAATTTTTTGGAACA
     P  K  D  L  K  K  P  R  G  K  K  C  F  F  V  K  F  F  G  T
 181 GAAGATCATGCCTGGATCAAAGTGGAACAGCTGAAGCCATATCATGCTCATAAAGAGGAA
     E  D  H  A  W  I  K  V  E  Q  L  K  P  Y  H  A  H  K  E  E
 241 ATGATAAAAATTAACAAGGGTAAACGATTCCAGCAAGCGGTAGATGCTGTCGAAGAGTTC
     M  I  K  I  N  K  G  K  R  F  Q  Q  A  V  D  A  V  E  E  F
 301 CTCAGGAGAGCCAAAGGGAAAGACCAGACGTCATCCCACAATTCTTCTGATGACAAGAAT
     L  R  R  A  K  G  K  D  Q  T  S  S  H  N  S  S  D  D  K  N
 361 CGACGTAATTCCAGTGAGGAGAGAAGTAGGCCAAACTCAGGTGATGAGAAGCGCAAACTT
     R  R  N  S  S  E  E  R  S  R  P  N  S  G  D  E  K  R  K  L
 421 AGCCTGTCTGAAGGGAAGGTGAAGAAGAACATGGGAGAAGGAAAGAAGAGGGTGTCTTCA
     S  L  S  E  G  K  V  K  K  N  M  G  E  G  K  K  R  V  S  S
 481 GGCTCTTCAGAGAGAGGCTCCAAATCCCCTCTGAAAAGAGCCCAAGAGCAAAGTCCCCGG
     G  S  S  E  R  G  S  K  S  P  L  K  R  A  Q  E  Q  S  P  R
 541 AAGCGGGGTCGGCCCCCAAAGGATGAGAAGGATCTCACCATCCCGGAGTCTAGTACCGTG
     K  R  G  R  P  P  K  D  E  K  D  L  T  I  P  E  S  S  T  V
 601 AAGGGGATGATGGCCGGACCGATGGCCGCGTTTAAATGGCAGCCAACCGCAAGCGAGCCT
     K  G  M  M  A  G  P  M  A  A  F  K  W  Q  P  T  A  S  E  P
 661 GTTAAAGATGCAGATCCTCATTTCCATCATTTCCTGCTAAGCCAAACAGAGAAGCCAGCT
     V  K  D  A  D  P  H  F  H  H  F  L  L  S  Q  T  E  K  P  A
 721 GTCTGTTACCAGGCAATCACGAAGAAGTTGAAAATATGTGAAGACCTCCTTCTTCCTAGG
     V  C  Y  Q  A  I  T  K  K  L  K  I  C  E  D  L  L  L  P  R
 781 TGAAGTGGGCAATGCAGCCAAGATGATGCTGATCGTGAACATGGTCCAAGGGAGCTTCAT
 841 GGCCACTATTGCCGAGGGGCTGACCCTGGCCCAGGTGACAGGCCAGTCCCAGCAGACACT
 901 CTTGGACATCCTCAATCAGGGACAGTTGGCCAGCATCTTCCTGGACCAGAAGTGCCAAAA
 961 TATCCTGCAAGGAAACTTTAAGCCTGATTTCTACCTGAAATACATTCAGAAGGATCTCCG
1021 CTTAGCCATTGCGCTGGGTGATGCGGTCAACCATCCGACTCCCATGGCAGCTGCAGCAAA
```

FIG. 1A

1081 TGAGGTGTACAAAAGAGCCAAGGCGCTGGACCAGTCTGACAACGATATGTCCGCCGTGTA
1141 CCGAGCCTACATACACTAAGCTGTCGACACCCCGCCCTCACCCCTCCAATCCCCCCTCTG
1201 ACCCCCTCTTCCTCACATGGGGTCGGGGGCCTGGGAGTTCATTCTGGTACCAGCCCACCT
1261 ATCTCCATTTCCTTTTATACAGACTTTGAGACTTGCCATCAGCACAGCACACAGCAGCAC
1321 CCTTCCCCTGAGGTCGGTGGGGAGGGGACAAGTGTCAGCAGGATTGGCGTGTGGGAAAGC
1381 TCTTGAGCTGGGCACTGGCCCCCCGGACGAGGTGGYTGTGTGTTCACACACACACACACA
1441 CACACACACACACACACACACACAGGCTCTCGCCCCAGGATAGAAGCTGCCCAGAAACTG
1501 CTGCCTGGCTTTTTTTCTTCCGAGCTTGTCTTATCTCAAACCCCTTCCAGTCAAGGAACT
1561 AGAATCAGCAACGAGAGTTGGAAGCCTTCCCACAGCTTCCCCCAGAGCGAAGAGGCTGTA
1621 GTCATGTCCCCATCCCCCACTGGATTCCCTACAAGGAGAGGCCTTGGGCCCAGATGAGCC
1681 AGTACAGACTCCAGACAGAGGGGCCCTTGGGGCCCTCCAACCTCAGGTGATGAGCTGAGA
1741 AAGATGTTCACGTCTAAGCGTCCAGTGTGCACCCAGCGCTCCATAGACGCCTTTGTGAAC
1801 TGAAAAGAGACTGGCAGAGTCCCGAGAAGATGGGGCCCTGGCTTTCCAGGGAGTGCAGCA
1861 AGCAGCCGGCCTGCAGGTGAGCATGGAGGCCCGGCCCTCACCGCCTCGAAGCCATGCCCC
1921 AGATGCCACTGCCACAGCGGGCGCTCGCTCCTCCCTAGGCTGTTTTAGTATTTGGATTTG
1981 CATTCCATCCCTTGGGAGGGAGTCCTCAGGGCCACTAGTGATGAGCCAAGAGGAGTGGGG
2041 GTTGGGGGCGCTCCTTTCTGTTTCCGTTAGGCCACAGACTCTTCACCTGGCTCTGACTTA
2101 CCTCGGTCCCCTCCCAGTGGTCCCACCTTCTCCACCCTGCCCTGCCAAGTCCCCTGCATG
2161 CCCACCGCTCTCCATCCTCCCTCCTCTCCCTCTTCCTCCCGTGGAGACAGTATTTCTTTC
2221 TGTCTGTCCCTTTGGCCCAGACCCAGCCTGACCAACGATGAGCATTTCTTAGGCTCAGCT
2281 CTTGATACGGAAACGAGTGTCTTCACTCCAGCCAGCATCATGGTCTTCGGTGCTTCCCGG
2341 GCCCGGGGTCTGTCGGGAGGGAAGAGAACTGGGCCTGACCTACCTGAACTGACTGGCCCT
2401 CCGAGGTGGGTCTGGGACATCCTAGAGGCCCTACATTTGTCCTTGGATAGGGGACCGGGG
2461 GGGGCTTGGAATGTTSCAAAAAAAAAAGTTACCCAAGGGATGTCAGTTTTTATCCCTCT
2521 GCATGGGTTGGATTTTCCAAAATCATAATTTGCAGAAGGAAGGCCAGCATTTACGATGCA
2581 ATATGTAATTATATATAGGGTGGCCACACTAGGGCGGGGTCCTTCCCCCCTCACAGCTTT
2641 GGCCCCTTTCAGAGATTAGAAACTGGGTTAGAGGATTGCAGAAGACGAGTGGGGGGAGGG
2701 CAGGGAAGATGCCTGTCGGGTTTTTAGCACAGTTCATTTCACTGGGATTTTGAAGCATTT
2761 CTGTCTGAACACAAAGCCTGTTCTAGTCCTGGCGGAACACACTGGGGGTGGGGGCGGGGG
2821 AAGATGCGGTAATGAAACCGGTTAGTCAATTTTGTCTTAATATTGTTGACAATTCTGTAA
2881 AGTTCCTTTTTATGAATATTTCTGTTTAAGCTATTTCACCTTTCTTTTGAAATCCTTCCC
2941 TTTTAAGGAGAAAATGTGACACTTTGTGAAAAAGCTTGTAAGAAAGCCCCTCCCTTTTTT
3001 CTTTAAACCTTTAAATGACAAATCTAGGTAATTAAGGTTGTGAATTTTTATTTTTGCTTT
3061 GTTTTTAATGAACATTTGTCTTTCAGAATAGGATTGTGTGATAATGTTTAAATGGSAAAA
3121 ACAAAACATGATTTTGTGCAATTAACAAAGCTACTGCAAGGAAAATAAAACACTTCTTGG
3181 TAACAAAAAAAAAAAAAAAAAA 3202

FIG. 1B

COMPARISON OF AMINO ACID SEQUENCES
BETWEEN HDGF-1 AND HDGF-2

```
                                                10        20        30
HDGF-2                                  MAAVSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRG
                                                ||||::|:  ||:||::| : |::  |: :
HDGF-1                              MSRSNRQKEYKCGDLVFAKMKGYPHWPARIDEMPEAAVKSTA

              40        50        60        70        80        90
HDGF-2        KKCFFVKFFGTEDHAWIKVEQLKPYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQ
              :| : | ||||:: |::  ::| ||:: ||:: | || | | ::: ::|:     : : :
HDGF-1        NK-YQVFFFGTHETAFLGPKDLFPYEESKEKFGKPNKRKGFSEGLWEIEN-----NPTVK

              100       110       120       130       140       150
HDGF-2        TSSHNSSDDKNRRNSSEERSRPNSGDEKRKLSLSEGKVKKNMGEGKKRVSSGSSERGSKS
              :|:::||::|:  :::|  : :::||:::| : :||: :   :|||  ::: ::|:::|:
HDGF-1        ASGYQSSQKKSCVEEPEPEPEAAEGDGDKK-GNAEGSSD---EEGKLVIDEPAKEKNEKG

              160       170       180       190       200       210
HDGF-2        PLKRAQEQSPRKRGRPPKDEKDLTIPESSTVKGMMAGPMA-AFKWQPTASEPVKDADPHF
              :||| :::   :: ::||:::: :  |:::::  :: |:: : : ::|:||| :: :|:
HDGF-1        ALKRRAGDLLEDSPKRPKEAENPEGEEKEAATLEVERPLPMEVEKNSTPSEPGSGRGPPQ

              220       230       240       250
HDGF-2        HHFLLSQTEKPAVCYQAITKKLKICEDLLLPR

HDGF-1        EEEEEEDEEEEATKEDAEAPGIRDHESL
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FIG. 2

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Nucleotide and Predicted Translation Product for Human Hepatoma Derived Growth Factor-Like Protein (HDGF-2)

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   1 GAATTCGTGCTCTTAGGGTGGTTGGGTGGTAAGATGGCGGCTGTGAGTCTGCGGCTCGGC
                                       M  A  A  V  S  L  R  L  G

  61 GACTTGGTGTGGGGAAACTCGGCCGATATCCTCCTTGGCCAGGAAAGATTGTTAATCCA
     D  L  V  W  G  K  L  G  R  Y  P  P  W  P  G  K  I  V  N  P

 121 CCAAAGGACTTGAAGAAACCTCGCGGAAAGAAATGCTTCTTTGTGAAATTTTTTGGAACA
     P  K  D  L  K  K  P  R  G  K  K  C  F  F  V  K  F  F  G  T

 181 GAAGATCATGCCTGGATCAAAGTGGAACAGCTGAAGCCATATCATGCTCATAAAGAGGAA
     E  D  H  A  W  I  K  V  E  Q  L  K  P  Y  H  A  H  K  E  E

 241 ATGATAAAAATTAACAAGGGTAAACGATTCCAGCAAGCGGTAGATGCTGTCGAAGAGTTC
     M  I  K  I  N  K  G  K  R  F  Q  Q  A  V  D  A  V  E  E  F

 301 CTCAGGAGAGCCAAAGGGAAAGACCAGACGTCATCCCACAATTCTTCTGATGACAAGAAT
     L  R  R  A  K  G  K  D  Q  T  S  S  H  N  S  S  D  D  K  N

 361 CGACGTAATTCCAGTGAGGAGAGAAGTAGGCCAAACTCAGGTGATGAGAAGCGCAAACTT
     R  R  N  S  S  E  E  R  S  R  P  N  S  G  D  E  K  R  K  L

 421 AGCCTGTCTGAAGGGAAGGTGAAGAAGAACATGGGAGAAGGAAAGAAGAGGGTGTCTTCA
     S  L  S  E  G  K  V  K  K  N  M  G  E  G  K  K  R  V  S  S

 481 GGCTCTTCAGAGAGAGGCTCCAAATCCCCTCTGAAAAGAGCCCAAGAGCAAAGTCCCCGG
     G  S  S  E  R  G  S  K  S  P  L  K  R  A  Q  E  Q  S  P  R

 541 AAGCGGGGTCGGCCCCCAAAGGATGAGAAGGATCTCACCATCCCGGAGTCTAGTACCGTG
     K  R  G  R  P  P  K  D  E  K  D  L  T  I  P  E  S  S  T  V

 601 AAGGGGATGATGGCCGGACCGATGGCCGCGTTTAAATGGCAGCCAACCGCAAGCGAGCCT
     K  G  M  M  A  G  P  M  A  A  F  K  W  Q  P  T  A  S  E  P

 661 GTTAAAGATGCAGATCCTCATTTCCATCATTTCCTGCTAAGCCAAACAGAGAAGCCAGCT
     V  K  D  A  D  P  H  F  H  H  F  L  L  S  Q  T  E  K  P  A

 721 GTCTGTTACCAGGCAATCACGAAGAAGTTGAAAATATGTGAAGACCTCCTTCTTCCTAGG
     V  C  Y  Q  A  I  T  K  K  L  K  I  C  E  D  L  L  L  P  R

 781 TGAAGTGGGCAATGCAGCCAAGATGATGCTGATCGTGAACATGGTCCAAGGGAGCTTCAT
 841 GGCCACTATTGCCGAGGGGCTGACCCTGGCCCAGGTGACAGGCCAGTCCCAGCAGACACT
 901 CTTGGACATCCTCAATCAGGGACAGTTGGCCAGCATCTTCCTGGACCAGAAGTGCCAAAA
 961 TATCCTGCAAGGAAACTTTAAGCCTGATTTCTACCTGAAATACATTCAGAAGGATCTCCG
1021 CTTAGCCATTGCGCTGGGTGATGCGGTCAACCATCCGACTCCCATGGCAGCTGCAGCAAA
1081 TGAGGTGTACAAAAGAGCCAAGGCGCTGGACCAGTCTGACAACGATATGTCCGCCGTGTA
1141 CCGAGCCTACATACACTAAGCTGTCGACACCCCGCCCTCACCCCTCCAATCCCCCCTCTG
1201 ACCCCCTCTTCCTCACATGGGGTCGGGGGCCTGGGAGTTCATTCTGGTACCAGCCCACCT
1261 ATCTCCATTTCCTTTTATACAGACTTTGAGACTTGCCATCAGCACAGCACACAGCAGCAC
1321 CCTTCCCCTGAGGTCGGTGGGGAGGGGACAAGTGTCAGCAGGATTGGCGTGTGGGAAAGC
1381 TCTTGAGCTGGGCACTGGCCCCCCGGACGAGGTGGYTGTGTGTTCACACACACACACACA
1441 CACACACACACACACACACACACAGGCTCTCGCCCCAGGATAGAAGCTGCCCAGAAACTG
```

FIGURE 1 1/2

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1501  CTGCCTGGCTTTTTTTCTTCCGAGCTTGTCTTATCTCAAACCCCTTCCAGTCAAGGAACT
1561  AGAATCAGCAACGAGAGTTGGAAGCCTTCCCACAGCTTCCCCCAGAGCGAAGAGGCTGTA
1621  GTCATGTCCCCATCCCCCACTGGATTCCCTACAAGGAGAGGCCTTGGGCCCAGATGAGCC
1681  AGTACAGACTCCAGACAGAGGGGCCCTTGGGGCCCTCCAACCTCAGGTGATGAGCTGAGA
1741  AAGATGTTCACGTCTAAGCGTCCAGTGTGCACCCAGCGCTCCATAGACGCCTTTGTGAAC
1801  TGAAAAGAGACTGGCAGAGTCCCGAGAAGATGGGGCCCTGGCTTTCCAGGGAGTGCAGCA
1861  AGCAGCCGGCCTGCAGGTGAGCATGGAGGCCCGGCCCTCACCGCCTCGAAGCCATGCCCC
1921  AGATGCCACTGCCACAGCGGGCGCTCGCTCCTCCCTAGGCTGTTTTAGTATTTGGATTTG
1981  CATTCCATCCCTTGGGAGGGAGTCCTCAGGGCCACTAGTGATGAGCCAAGAGGAGTGGGG
2041  GTTGGGGGCGCTCCTTTCTGTTTCCGTTAGGCCACAGACTCTTCACCTGGCTCTGACTTA
2101  CCTCGGTCCCCTCCCAGTGGTCCCACCTTCTCCACCCTGCCCTGCCAAGTCCCCTGCATG
2161  CCCACCGCTCTCCATCCTCCTCCTCTCCCTCTTCCTCCCGTGGAGACAGTATTTCTTTC
2221  TGTCTGTCCCTTTGGCCCAGACCCAGCCTGACCAACGATGAGCATTTCTTAGGCTCAGCT
2281  CTTGATACGGAAACGAGTGTCTTCACTCCAGCCAGCATCATGGTCTTCGGTGCTTCCCGG
2341  GCCCGGGGTCTGTCGGGAGGGAAGAGAACTGGGCCTGACCTACCTGAACTGACTGGCCCT
2401  CCGAGGTGGGTCTGGGACATCCTAGAGGCCCTACATTTGTCCTTGGATAGGGGACCGGGG
2461  GGGGCTTGGAATGTTSCAAAAAAAAAAAGTTACCCAAGGGATGTCAGTTTTTTATCCCTCT
2521  GCATGGGTTGGATTTTCCAAAATCATAATTTGCAGAAGGAAGGCCAGCATTTACGATGCA
2581  ATATGTAATTATATATAGGGTGGCCACACTAGGGCGGGGTCCTTCCCCCCTCACAGCTTT
2641  GGCCCCTTTCAGAGATTAGAAACTGGGTTAGAGGATTGCAGAAGACGAGTGGGGGGAGGG
2701  CAGGGAAGATGCCTGTCGGGTTTTTAGCAAAGTTCATTTCACTGGGATTTTGAAGCATTT
2761  CTGTCTGAACACAAAGCCTGTTCTAGTCCTGGCGGAACACACTGGGGGTGGGGGCGGGGG
2821  AAGATGCGGTAATGAAACCGGTTAGTCAATTTTGTCTTAATATTGTTGACAATTCTGTAA
2881  AGTTCCTTTTTATGAATATTTCTGTTTAAGCTATTTCACCTTTCTTTTGAAATCCTTCCC
2941  TTTTAAGGAGAAAATGTGACACTTTGTGAAAAAGCTTGTAAGAAAGCCCCTCCCTTTTTT
3001  CTTTAAACCTTTAAATGACAAATCTAGGTAATTAAGGTTGTGAATTTTTATTTTTGCTTT
3061  GTTTTTAATGAACATTTGTCTTTCAGAATAGGATTGTGTGATAATGTTTAAATGGSAAAA
3121  ACAAAACATGATTTTGTGCAATTAACAAAGCTACTGCAAGGAAAATAAAACACTTCTTGG
3181  TAACAAAAAAAAAAAAAAAAA  3202
```

FIGURE 1 2/2

Comparis n f Amin Acid Sequences Between HDGF-1 and HDGF-2

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                                          10        20        30
HDGF-2                           MAAVSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRG
                                         ||||::|:  ||:||::| : |::  |: :
HDGF-1                       MSRSNRQKEYKCGDLVFAKMKGYPHWPARIDEMPEAAVKSTA

           40        50        60        70        80        90
HDGF-2     KKCFFVKFFGTEDHAWIKVEQLKPYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQ
           :| : | ||||:: |::  ::| ||:: ||:: | || | | ::: ::|:     : : :
HDGF-1     NK-YQVFFFGTHETAFLGPKDLFPYEESKEKFGKPNKRKGFSEGLWEIEN-----NPTVK

           100       110       120       130       140       150
HDGF-2     TSSHNSSDDKNRRNSSEERSRPNSGDEKRKLSLSEGKVKKNMGEGKKRVSSGSSERGSKS
           :|:::||::|:  :::|  : :::||:::| : :||: :   :|||  ::: ::|:::|:
HDGF-1     ASGYQSSQKKSCVEEPEPEPEAAEGDGDKK-GNAEGSSD---EEGKLVIDEPAKEKNEKG

           160       170       180       190       200       210
HDGF-2     PLKRAQEQSPRKRGRPPKDEKDLTIPESSTVKGMMAGPMA-AFKWQPTASEPVKDADPHF
           :||| :::   :: ::||:::: :  |:::::  :: |:: : : ::|:||| :: :|:
HDGF-1     ALKRRAGDLLEDSPKRPKEAENPEGEEKEAATLEVERPLPMEVEKNSTPSEPGSGRGPPQ

           220       230       240       250
HDGF-2     HHFLLSQTEKPAVCYQAITKKLKICEDLLLPR

HDGF-1     EEEEEEDEEEEATKEDAEAPGIRDHESL
```

FIGURE 2 1/1